

Sequence Listing

<110> Ernst-Moritz-Arndt Universität Greifswald

<120> Modulation of the Synthesis of Insulin

<130> P 64322

<160> 12

<170> PatentIn version 3.1

<210> 1

<211> 852

<212> DNA

<213> Homo sapiens

<220>

<221> Stop codon

<222> (850)..(852)

<223> Nucleotide sequence of PDX-1

<400> 1

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cagcgaggcc cggcgccgga gttcagcgcc agccccctg cgtgcctgta catgggccgc	120
cagccccgc cgccgccgcc gcaccggttc cctggcgccc tgggcgcgct ggagcagggc	180
agcccccg acatctcccc gtacgaggtg cccccctcg ccgacgaccc cgcggtggcg	240
caccttcacc accacctccc ggctcagctc gcgctcccc acccgcccgc cgggcccttc	300
cgggagggag ccgagccggg cgtcctggag gagcccaacc gcgtccagct gcctttccca	360
tggatgaagt ctaccaaagc tcacgcgtgg aaaggccagt gggcaggcgg cgcctacgct	420
gcggagccgg aggagaacaa gcggacgcgc acggcctaca cgcgcgcaca gctgctagag	480
ctggagaagg agttcctatt caacaagtac atctcacggc cgcgccgggt ggagctggct	540
gtcatgttga acttgaccga gagacacatc aagatctggt tccaaaaccg ccgcatgaag	600
tggaaaaagg aggaggacaa gaagcgcggc ggcgggacag ctgtcggggg tggcggggtc	660
gcggagcctg agcaggactg cgccgtgacc tccggcgagg agcttctggc gctgccgccg	720
ccgccgccc ccggagggtg tgtgccgcc gctgccccg ttgccgccc agagggccgc	780
ctgccgcctg gccttagcgc gtcgccacag ccctccagcg tcgcgcctcg gcggccgcag	840
gaaccacgat ga	852

<210> 2  
<211> 283  
<212> PRT  
<213> Homo sapiens

<223> Amino acid sequence of PDX-1

<400> 2  
Met Asn Gly Glu Glu Gln Tyr Tyr Ala Ala Thr Gln Leu Tyr Lys Asp  
1 5 10 15  
  
Pro Cys Ala Phe Gln Arg Gly Pro Ala Pro Glu Phe Ser Ala Ser Pro  
20 25 30  
  
Pro Ala Cys Leu Tyr Met Gly Arg Gln Pro Pro Pro Pro Pro Pro His  
35 40 45  
  
Pro Phe Pro Gly Ala Leu Gly Ala Leu Glu Gln Gly Ser Pro Pro Asp  
50 55 60  
  
Ile Ser Pro Tyr Glu Val Pro Pro Leu Ala Asp Asp Pro Ala Val Ala  
65 70 75 80  
  
His Leu His His His Leu Pro Ala Gln Leu Ala Leu Pro His Pro Pro  
85 90 95  
  
Ala Gly Pro Phe Pro Glu Gly Ala Glu Pro Gly Val Leu Glu Glu Pro  
100 105 110  
  
Asn Arg Val Gln Leu Pro Phe Pro Trp Met Lys Ser Thr Lys Ala His  
115 120 125  
  
Ala Trp Lys Gly Gln Trp Ala Gly Gly Ala Tyr Ala Ala Glu Pro Glu  
130 135 140  
  
Glu Asn Lys Arg Thr Arg Thr Ala Tyr Thr Arg Ala Gln Leu Leu Glu  
145 150 155 160  
  
Leu Glu Lys Glu Phe Leu Phe Asn Lys Tyr Ile Ser Arg Pro Arg Arg  
165 170 175  
  
Val Glu Leu Ala Val Met Leu Asn Leu Thr Glu Arg His Ile Lys Ile  
180 185 190  
  
Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys Glu Glu Asp Lys Lys  
195 200 205

Arg Gly Gly Gly Thr Ala Val Gly Gly Gly Gly Val Ala Glu Pro Glu  
 210 215 220

Gln Asp Cys Ala Val Thr Ser Gly Glu Glu Leu Leu Ala Leu Pro Pro  
 225 230 235 240

Pro Pro Pro Pro Gly Gly Ala Val Pro Pro Ala Ala Pro Val Ala Ala  
 245 250 255

Arg Glu Gly Arg Leu Pro Pro Gly Leu Ser Ala Ser Pro Gln Pro Ser  
 260 265 270

Ser Val Ala Pro Arg Arg Pro Gln Glu Pro Arg  
 275 280

<210> 3  
 <211> 1182  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> Stop codon  
 <222> (1080)..(1082)  
 <223> Nucleotide sequence of CK II alpha subunit

<400> 3  
 atgtcgggac ccgtgccaaag cagggccaga gtttacacag atgttaatac acacagacct 60  
 cgagaataact gggattacga gtcacatgtg gtggaatggg gaaatcaaga tgactaccag 120  
 ctggttcgaa aattaggccg aggtaaatac agtgaagtat ttgaagccat caacatcaca 180  
 aataatgaaa aagttgttgt taaaattctc aagccagtaa aaaagaagaa aattaagcgt 240  
 gaaataaaga ttttgagaga tttgagagga ggtcccaaca tcatcacact ggcagacatt 300  
 gtaaaagacc ctgtgtcacg aacccccgcc ttgggttttg aacacgtaaa caacacagac 360  
 ttcaagcaat tgtaccagac gttacagac tatgatattc gattttacat gtatgagatt 420  
 ctgaaggccc tggattattg tcacagcatg ggaattatgc acagagatgt caagccccat 480  
 aatgtcatga ttgatcatga gcacagaaag ctacgactaa tagactgggg tttggctgag 540  
 ttttatcatc ctggccaaga atataatgtc cgagttgctt cccgatactt caaaggctcct 600  
 gagctacttg tagactatca gatgtacgat tatagtttgg atatgtggag tttgggttgt 660  
 atgctggcaa gtatgatctt tcggaaggag ccatttttcc atggacatga caattatgat 720  
 cagttggtga ggatagccaa ggttctgggg acagaagatt tatatgacta tattgacaaa 780  
 tacaacattg aattagatcc acgtttcaat gatatcttgg gcagacactc tcgaaagcga 840  
 tgggaacgct ttgtccacag tgaaaatcag caccttgtca gccctgaggc cttggatttc 900  
 ctggacaaac tgctgcgata tgaccaccag tcacggctta ctgcaagaga ggcaatggag 960

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caccctatt tctacactgt tgtgaaggac caggctcgaa tgggttcac tagcatgcc 1020
gggggcagta cgcccgtcag cagcgccaat atgatgtcag ggattttctt agtgccaacc 1080
ccttcacccc ttggacctct ggcaggctca ccagtgattg ctgctgccaa ccccttggg 1140
atgcctgttc cagctgccgc tggcgctcag cagtaacggc cc 1182

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<210> 4
<211> 391
<212> PRT
<213> Homo sapiens

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<223> Amino acid sequence of CKII alpha subunit

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<400> 4
Met Ser Gly Pro Val Pro Ser Arg Ala Arg Val Tyr Thr Asp Val Asn
1          5          10          15

Thr His Arg Pro Arg Glu Tyr Trp Asp Tyr Glu Ser His Val Val Glu
          20          25          30

Trp Gly Asn Gln Asp Asp Tyr Gln Leu Val Arg Lys Leu Gly Arg Gly
          35          40          45

Lys Tyr Ser Glu Val Phe Glu Ala Ile Asn Ile Thr Asn Asn Glu Lys
50          55          60

Val Val Val Lys Ile Leu Lys Pro Val Lys Lys Lys Ile Lys Arg
65          70          75          80

Glu Ile Lys Ile Leu Glu Asn Leu Arg Gly Gly Pro Asn Ile Ile Thr
          85          90          95

Leu Ala Asp Ile Val Lys Asp Pro Val Ser Arg Thr Pro Ala Leu Val
100          105          110

Phe Glu His Val Asn Asn Thr Asp Phe Lys Gln Leu Tyr Gln Thr Leu
115          120          125

Thr Asp Tyr Asp Ile Arg Phe Tyr Met Tyr Glu Ile Leu Lys Ala Leu
130          135          140

Asp Tyr Cys His Ser Met Gly Ile Met His Arg Asp Val Lys Pro His
145          150          155          160

Asn Val Met Ile Asp His Glu His Arg Lys Leu Arg Leu Ile Asp Trp
          165          170          175

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Gly Leu Ala Glu Phe Tyr His Pro Gly Gln Glu Tyr Asn Val Arg Val  
180 185 190

Ala Ser Arg Tyr Phe Lys Gly Pro Glu Leu Leu Val Asp Tyr Gln Met  
195 200 205

Tyr Asp Tyr Ser Leu Asp Met Trp Ser Leu Gly Cys Met Leu Ala Ser  
210 215 220

Met Ile Phe Arg Lys Glu Pro Phe Phe His Gly His Asp Asn Tyr Asp  
225 230 235 240

Gln Leu Val Arg Ile Ala Lys Val Leu Gly Thr Glu Asp Leu Tyr Asp  
245 250 255

Tyr Ile Asp Lys Tyr Asn Ile Glu Leu Asp Pro Arg Phe Asn Asp Ile  
260 265 270

Leu Gly Arg His Ser Arg Lys Arg Trp Glu Arg Phe Val His Ser Glu  
275 280 285

Asn Gln His Leu Val Ser Pro Glu Ala Leu Asp Phe Leu Asp Lys Leu  
290 295 300

Leu Arg Tyr Asp His Gln Ser Arg Leu Thr Ala Arg Glu Ala Met Glu  
305 310 315 320

His Pro Tyr Phe Tyr Thr Val Val Lys Asp Gln Ala Arg Met Gly Ser  
325 330 335

Ser Ser Met Pro Gly Gly Ser Thr Pro Val Ser Ser Ala Asn Met Met  
340 345 350

Ser Gly Ile Ser Ser Val Pro Thr Pro Ser Pro Leu Gly Pro Leu Ala  
355 360 365

Gly Ser Pro Val Ile Ala Ala Ala Asn Pro Leu Gly Met Pro Val Pro  
370 375 380

Ala Ala Ala Gly Ala Gln Gln  
385 390

<210> 5  
<211> 1053  
<212> DNA  
<213> Homo sapiens

<220>  
<221> Stop codon  
<222> (1051)..(1053)  
<223> Nucleotide sequence of CKII alpha' subunit

<400> 5  
atgcccggcc cggccgcggg cagcagggcc cgggtctacg ccgaggtgaa cagtctgagg 60  
agccgcgagt actgggacta cgaggctcac gtcccgagct ggggtaatca agatgattac 120  
caactggttc gaaaacttgg tcggggaaaa tatagtgaag tatttgaggc cattaatatc 180  
accaacaatg agagagtggg tgtaaaaatc ctgaagccag tgaagaaaaa gaagataaaa 240  
cgagaggtta agattctgga gaaccttcgt ggtggaacaa atatcattaa gctgattgac 300  
actgtaaagg accccgtgtc aaagacacca gctttggtat ttgaatatat caataatata 360  
gattttaagc aactctacca gatcctgaca gactttgata tccggtttta tatgtatgaa 420  
ctacttaaag ctctggatta ctgccacagc aagggaatca tgcacaggga tgtgaaacct 480  
cacaatgtca tgatagatca ccaacagaaa aagctgcgac tgatagattg gggctctggca 540  
gaattctatc atcctgctca ggagtacaat gttcgtgtag cctcaaggta cttcaaggga 600  
ccagagctcc tcgtggacta tcagatgtat gattatagct tggacatgtg gagtttgggc 660  
tgtatgttag caagcatgat ctttcgaagg gaaccattct tccatggaca ggacaactat 720  
gaccagcttg ttcgcattgc caaggttctg ggtacagaag aactgtatgg gtatctgaag 780  
aagtatcaca tagacctaga tccacacttc aacgatatcc tgggacaaca ttcacggaaa 840  
cgctgggaaa actttatcca tagtgagaac agacaccttg tcagccctga ggccttagat 900  
cttctggaca aacttctgcg atacgaccat caacagagac tgactgccaag agaggccatg 960  
gagcaccat acttctaccc tgttgtgaag gagcagtcctc agccttgtgc agacaatgct 1020  
gtgctttcca gtggtctcac ggcagcacga tga 1053

<210> 6  
<211> 350  
<212> PRT  
<213> Homo sapiens  
<223> Amino acid sequence of CK II alpha' subunit

&lt;400&gt; 6

Met Pro Gly Pro Ala Ala Gly Ser Arg Ala Arg Val Tyr Ala Glu Val  
1 5 10 15

Asn Ser Leu Arg Ser Arg Glu Tyr Trp Asp Tyr Glu Ala His Val Pro  
20 25 30

Ser Trp Gly Asn Gln Asp Asp Tyr Gln Leu Val Arg Lys Leu Gly Arg  
35 40 45

Gly Lys Tyr Ser Glu Val Phe Glu Ala Ile Asn Ile Thr Asn Asn Glu  
50 55 60

Arg Val Val Val Lys Ile Leu Lys Pro Val Lys Lys Lys Lys Ile Lys  
65 70 75 80

Arg Glu Val Lys Ile Leu Glu Asn Leu Arg Gly Gly Thr Asn Ile Ile  
85 90 95

Lys Leu Ile Asp Thr Val Lys Asp Pro Val Ser Lys Thr Pro Ala Leu  
100 105 110

Val Phe Glu Tyr Ile Asn Asn Thr Asp Phe Lys Gln Leu Tyr Gln Ile  
115 120 125

Leu Thr Asp Phe Asp Ile Arg Phe Tyr Met Tyr Glu Leu Leu Lys Ala  
130 135 140

Leu Asp Tyr Cys His Ser Lys Gly Ile Met His Arg Asp Val Lys Pro  
145 150 155 160

His Asn Val Met Ile Asp His Gln Gln Lys Lys Leu Arg Leu Ile Asp  
165 170 175

Trp Gly Leu Ala Glu Phe Tyr His Pro Ala Gln Glu Tyr Asn Val Arg  
180 185 190

Val Ala Ser Arg Tyr Phe Lys Gly Pro Glu Leu Leu Val Asp Tyr Gln  
195 200 205

Met Tyr Asp Tyr Ser Leu Asp Met Trp Ser Leu Gly Cys Met Leu Ala  
210 215 220

Ser Met Ile Phe Arg Arg Glu Pro Phe Phe His Gly Gln Asp Asn Tyr  
225 230 235 240

Asp Gln Leu Val Arg Ile Ala Lys Val Leu Gly Thr Glu Glu Leu Tyr  
245 250 255

Gly Tyr Leu Lys Lys Tyr His Ile Asp Leu Asp Pro His Phe Asn Asp  
260 265 270

Ile Leu Gly Gln His Ser Arg Lys Arg Trp Glu Asn Phe Ile His Ser  
275 280 285

Glu Asn Arg His Leu Val Ser Pro Glu Ala Leu Asp Leu Leu Asp Lys  
290 295 300

Leu Leu Arg Tyr Asp His Gln Gln Arg Leu Thr Ala Lys Glu Ala Met  
305 310 315 320

Glu His Pro Tyr Phe Tyr Pro Val Val Lys Glu Gln Ser Gln Pro Cys  
325 330 335

Ala Asp Asn Ala Val Leu Ser Ser Gly Leu Thr Ala Ala Arg  
340 345 350

<210> 7  
<211> 648  
<212> DNA  
<213> Homo sapiens

<220>  
<221> Stop codon  
<222> (646)..(648)  
<223> Nucleotide sequence of CK II beta subunit

<400> 7  
atgagcagct cagaggaggt gtcttgatt tcttggttct gtgggctccg tggcaatgaa 60  
ttcttctgtg aagtggatga agactacatc caggacaaat ttaatcttac tggactcaat 120  
gagcaggtcc ctactatcgc acaagctcta gacatgatct tggacctgga gcctgatgaa 180  
gaactggaag acaaccccaa ccagagtgc ctgattgagc aggcagccga gatgctttat 240  
ggattgatcc acgcccgccta catccttacc aaccgtggca tcgcccagat gttggaaaag 300  
taccagcaag gagacttttg ttactgtcct cgtgtgtact gtgagaacca gccaatgctt 360  
cccattggcc ttccagacat ccaggtgaa gccatggtga agctctactg cccaagtgc 420  
atggatgtgt acacacccaa gtcacaaaga caccatcaca cggatggcgc ctacttcggc 480  
actggtttcc ctacatgct cttcatggtg catcccgagt accggcccaa gagacctgcc 540  
aaccagtttg tgcccaggct ctacggtttc aagatccatc cgatggccta ccagctgcag 600  
ctccaagccg ccagcaactt caagagccca gtcaagacga ttcgctga 648



<210> 8  
<211> 215  
<212> PRT  
<213> Homo sapiens

<223> Amino acid sequence of CK II beta subunit

<400> 8

Met Ser Ser Ser Glu Glu Val Ser Trp Ile Ser Trp Phe Cys Gly Leu  
1 5 10 15

Arg Gly Asn Glu Phe Phe Cys Glu Val Asp Glu Asp Tyr Ile Gln Asp  
20 25 30

Lys Phe Asn Leu Thr Gly Leu Asn Glu Gln Val Pro His Tyr Arg Gln  
35 40 45

Ala Leu Asp Met Ile Leu Asp Leu Glu Pro Asp Glu Glu Leu Glu Asp  
50 55 60

Asn Pro Asn Gln Ser Asp Leu Ile Glu Gln Ala Ala Glu Met Leu Tyr  
65 70 75 80

Gly Leu Ile His Ala Arg Tyr Ile Leu Thr Asn Arg Gly Ile Ala Gln  
85 90 95

Met Leu Glu Lys Tyr Gln Gln Gly Asp Phe Gly Tyr Cys Pro Arg Val  
100 105 110

Tyr Cys Glu Asn Gln Pro Met Leu Pro Ile Gly Leu Ser Asp Ile Pro  
115 120 125

Gly Glu Ala Met Val Lys Leu Tyr Cys Pro Lys Cys Met Asp Val Tyr  
130 135 140

Thr Pro Lys Ser Ser Arg His His His Thr Asp Gly Ala Tyr Phe Gly  
145 150 155 160

Thr Gly Phe Pro His Met Leu Phe Met Val His Pro Glu Tyr Arg Pro  
165 170 175

Lys Arg Pro Ala Asn Gln Phe Val Pro Arg Leu Tyr Gly Phe Lys Ile  
180 185 190

His Pro Met Ala Tyr Gln Leu Gln Leu Gln Ala Ala Ser Asn Phe Lys  
 195 200 205

Ser Pro Val Lys Thr Ile Arg  
 210 215

<210> 9  
 <211> 768  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> Stop codon  
 <222> (766)..(768)  
 <223> Nucleotide sequence of 14-3-3 epsilon

<400> 9  
 atggatgatac gagaggatct ggtgtaccag gcgaagctgg ccgagcaggc tgagcgatac 60  
 gacgaaatgg tggagtcaat gaagaaagta gcagggatgg atgtggagct gacagttgaa 120  
 gaaagaaacc tcctatctgt tgcataaag aatgtgattg gagctagaag agcctcctgg 180  
 agaataatca gcagcattga acagaaagaa gaaaacaagg gaggagaaga caagctaaaa 240  
 atgattcggg aatatcggca aatggttgag actgagctaa agttaatctg ttgtgacatt 300  
 ctggatgtac tggacaaaaca cctcattcca gcagctaaca ctggcgagtc caaggttttc 360  
 tattataaaa tgaaagggga ctaccacagg tatctggcag aatttgccac aggaaacgac 420  
 aggaaggagg ctgcggagaa cagcctagtg gcttataaag ctgctagtga tattgcaatg 480  
 acagaacttc caccaacgca tcctattcgc ttaggtcttg ctctcaattt ttccgtattc 540  
 tactacgaaa ttcttaattc ccctgaccgt gcctgcaggt tggcaaaagc agcttttgat 600  
 gatgcaattg cagaactgga tacgctgagt gaagaaagct ataaggactc tacacttatc 660  
 atgcagttgt tacgtgataa tctgacacta tggacttcag acatgcaggg tgacggtgaa 720  
 gacgagaata aagaagcgct gcaggacgtg gaagacgaaa atcagtga 768

<210> 10  
 <211> 255  
 <212> PRT  
 <213> Homo sapiens

<223> Amino acid sequence of 14-3-3 epsilon

<400> 10  
 Met Asp Asp Arg Glu Asp Leu Val Tyr Gln Ala Lys Leu Ala Glu Gln  
 1 5 10 15

Ala Glu Arg Tyr Asp Glu Met Val Glu Ser Met Lys Lys Val Ala Gly  
 20 25 30

Met Asp Val Glu Leu Thr Val Glu Glu Arg Asn Leu Leu Ser Val Ala  
 35 40 45

Tyr Lys Asn Val Ile Gly Ala Arg Arg Ala Ser Trp Arg Ile Ile Ser  
 50 55 60

Ser Ile Glu Gln Lys Glu Glu Asn Lys Gly Gly Glu Asp Lys Leu Lys  
 65 70 75 80

Met Ile Arg Glu Tyr Arg Gln Met Val Glu Thr Glu Leu Lys Leu Ile  
 85 90 95

Cys Cys Asp Ile Leu Asp Val Leu Asp Lys His Leu Ile Pro Ala Ala  
 100 105 110

Asn Thr Gly Glu Ser Lys Val Phe Tyr Tyr Lys Met Lys Gly Asp Tyr  
 115 120 125

His Arg Tyr Leu Ala Glu Phe Ala Thr Gly Asn Asp Arg Lys Glu Ala  
 130 135 140

Ala Glu Asn Ser Leu Val Ala Tyr Lys Ala Ala Ser Asp Ile Ala Met  
 145 150 155 160

Thr Glu Leu Pro Pro Thr His Pro Ile Arg Leu Gly Leu Ala Leu Asn  
 165 170 175

Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn Ser Pro Asp Arg Ala Cys  
 180 185 190

Arg Leu Ala Lys Ala Ala Phe Asp Asp Ala Ile Ala Glu Leu Asp Thr  
 195 200 205

Leu Ser Glu Glu Ser Tyr Lys Asp Ser Thr Leu Ile Met Gln Leu Leu  
 210 215 220

Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp Met Gln Gly Asp Gly Glu  
 225 230 235 240

Glu Gln Asn Lys Glu Ala Leu Gln Asp Val Glu Asp Glu Asn Gln  
 245 250 255

<210> 11  
<211> 1284  
<212> DNA  
<213> Homo sapiens

<220>  
<221> Stop codon  
<222> (1282)..(1284)  
<223> Nucleotide sequence of the short isoform of EED

<400> 11  
atgcttgccg ccaagaagca gaagctgagc agtgacgaga acagcaatcc agaactctct 60  
ggagacgaga atgatgacgc tgtcagtata gaaagtggta caaacactga acgccctgat 120  
acacctacaa acacgccaaa tgcacctgga agggaaaaggt ggggaaaagg aaaatggaag 180  
tcaaagaaat gcaaataattc tttcaaagt gttaaagtc tcaaggaaga tcataaccaa 240  
ccattgtttg gagttcagtt taactggcac agtaaagaag gagatccatt agtgtttgca 300  
actgtaggaa gcaacagagt taccttgtat gaatgtcatt cacaaggaga aatccggttg 360  
ttgcaatctt acgtggatgc tgatgctgat gaaaactttt acacttgtgc atggacctat 420  
gatagcaata cgagccatcc tctgctggct gtagctggat ctagaggcat aattaggata 480  
ataaatccta taacaatgca gtgtataaag cactatgttg gccatggaaa tgctatcaat 540  
gagctgaaat tccatccaag agatccaaat cttctcctgt cagtaagtaa agatcatgct 600  
ttacgattat ggaatatcca gacggacact ctggtggcaa ttttggagg cgtagaaggg 660  
cacagagatg aagttctaag tgctgattat gatcttttgg gtgaaaaaat aatgtcctgt 720  
ggtatggatc attctcttaa actttggagg atcaattcaa agagaatgat gaatgcaatt 780  
aaggaatctt atgattataa tccaaataaa actaacaggc catttatctc tcagaaaatc 840  
cattttcctg atttttctac cagagacata cataggaatt atgttgattg tgtgcgatgg 900  
ttaggcgatt tgatactttc taagtcttgt gaaaatgcca ttgtgtgctg gaaacctggc 960  
aagatggaag atgatataga taaaattaaa ccagtgat ctaatgtgac tattcttggg 1020  
cgatttgatt acagccagtg tgacatttgg tacatgaggt tttctatgga tttctggcaa 1080  
aagatgcttg cattgggcaa tcaagttggc aaactttatg tttgggattt agaagtagaa 1140  
gatcctcata aagccaaatg tacaacactg actcatcata aatgtgggtg tgctattcga 1200  
caaaccagtt ttagcaggga tagcagcatt cttatagctg tttgtgatga tgccagtatt 1260  
tggcgctggg atcgacttcg ataa 1284

<210> 12  
<211> 427  
<212> PRT  
<213> Homo sapiens

<223> Amino acid sequence of the short isoform of EED

<400> 12

Met Pro Ala Ala Lys Lys Gln Lys Leu Ser Ser Asp Glu Asn Ser Asn  
1 5 10 15

Pro Glu Leu Ser Gly Asp Glu Asn Asp Asp Ala Val Ser Ile Glu Ser  
20 25 30

Gly Thr Asn Thr Glu Arg Pro Asp Thr Pro Thr Asn Thr Pro Asn Ala  
35 40 45

Pro Gly Arg Lys Ser Trp Gly Lys Gly Lys Trp Lys Ser Lys Lys Cys  
50 55 60

Lys Tyr Ser Phe Lys Cys Val Asn Ser Leu Lys Glu Asp His Asn Gln  
65 70 75 80

Pro Leu Phe Gly Val Gln Phe Asn Trp His Ser Lys Glu Gly Asp Pro  
85 90 95

Leu Val Phe Ala Thr Val Gly Ser Asn Arg Val Thr Leu Tyr Glu Cys  
100 105 110

His Ser Gln Gly Glu Ile Arg Leu Leu Gln Ser Tyr Val Asp Ala Asp  
115 120 125

Ala Asp Glu Asn Phe Tyr Thr Cys Ala Trp Thr Tyr Asp Ser Asn Thr  
130 135 140

Ser His Pro Leu Leu Ala Val Ala Gly Ser Arg Gly Ile Ile Arg Ile  
145 150 155 160

Ile Asn Pro Ile Thr Met Gln Cys Ile Lys His Tyr Val Gly His Gly  
165 170 175

Asn Ala Ile Asn Glu Leu Lys Phe His Pro Arg Asp Pro Asn Leu Leu  
180 185 190

Leu Ser Val Ser Lys Asp His Ala Leu Arg Leu Trp Asn Ile Gln Thr  
195 200 205

Asp Thr Leu Val Ala Ile Phe Gly Gly Val Glu Gly His Arg Asp Glu  
210 215 220

Val Leu Ser Ala Asp Tyr Asp Leu Leu Gly Glu Lys Ile Met Ser Cys  
225 230 235 240

Gly Met Asp His Ser Leu Lys Leu Trp Arg Ile Asn Ser Lys Arg Met  
245 250 255

Met Asn Ala Ile Lys Glu Ser Tyr Asp Tyr Asn Pro Asn Lys Thr Asn  
260 265 270

Arg Pro Phe Ile Ser Gln Lys Ile His Phe Pro Asp Phe Ser Thr Arg  
275 280 285

Asp Ile His Arg Asn Tyr Val Asp Cys Val Arg Trp Leu Gly Asp Leu  
290 295 300

Ile Leu Ser Lys Ser Cys Glu Asn Ala Ile Val Cys Trp Lys Pro Gly  
305 310 315 320

Lys Met Glu Asp Asp Ile Asp Lys Ile Lys Pro Ser Glu Ser Asn Val  
325 330 335

Thr Ile Leu Gly Arg Phe Asp Tyr Ser Gln Cys Asp Ile Trp Tyr Met  
340 345 350

Arg Phe Ser Met Asp Phe Trp Gln Lys Met Leu Ala Leu Gly Asn Gln  
355 360 365

Val Gly Lys Leu Tyr Val Trp Asp Leu Glu Val Glu Asp Pro His Lys  
370 375 380

Ala Lys Cys Thr Thr Leu Thr His His Lys Cys Gly Ala Ala Ile Arg  
385 390 395 400

Gln Thr Ser Phe Ser Arg Asp Ser Ser Ile Leu Ile Ala Val Cys Asp  
405 410 415

Asp Ala Ser Ile Trp Arg Trp Asp Arg Leu Arg  
420 425